The crystal structure of a hyperthermoactive exopolygalacturonase from Thermotoga maritima reveals a unique tetramer

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Supplementary data

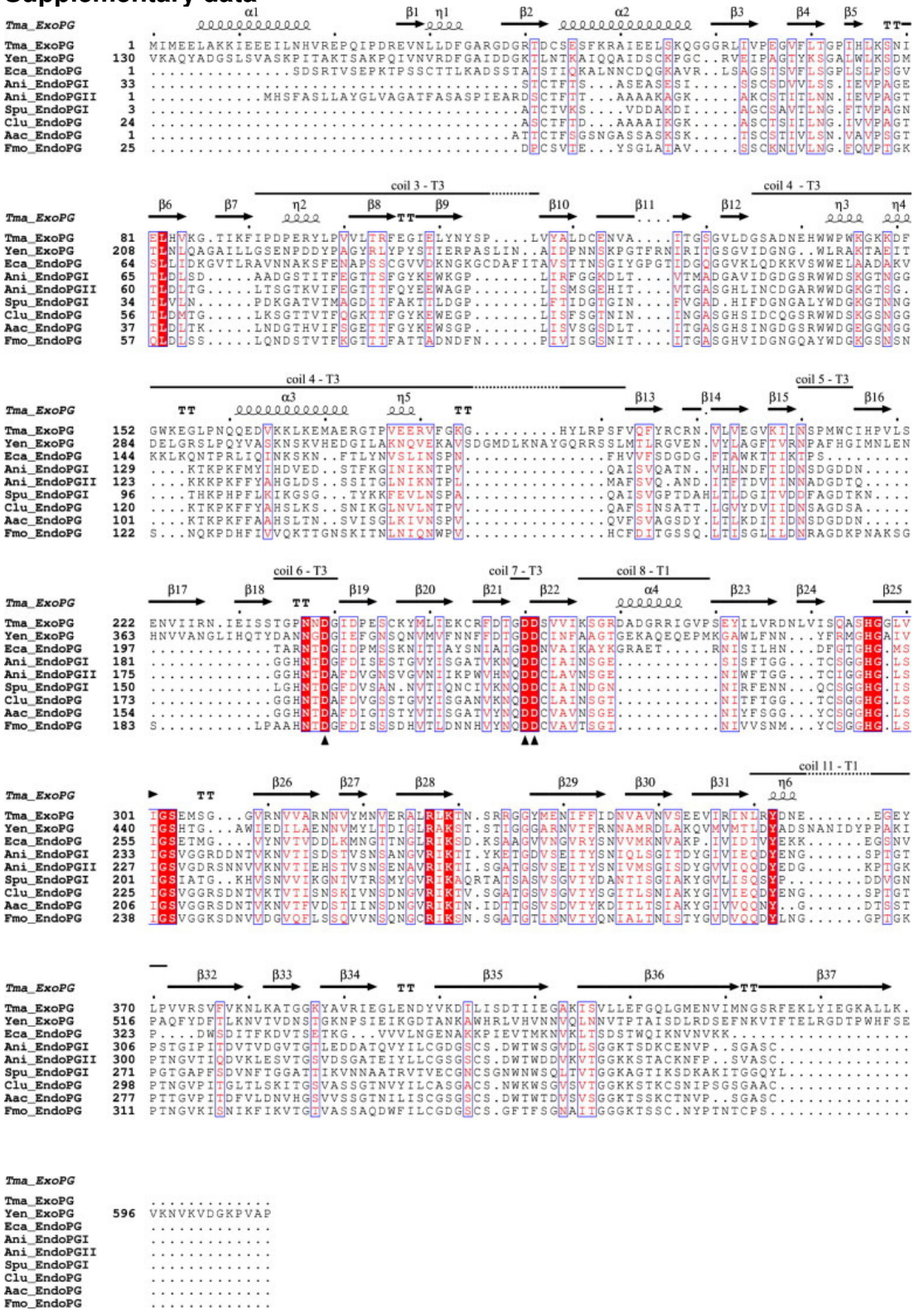

Fig. S1. Sequence alignment of polygalacturonases, figure prepared by ESPript. *Tma* = *Thermotoga maritima*, *Yen* = *Yersinia enterocolitica* (β-helical domain), *Eca* = *Erwinia carotovora*, *Ani* = *Aspergillus niger*, *Spu* = *Sterum purpureum*, *Clu* = *Colletotrichum lupine*, *Aac* = *Aspergillus aculeatus*, *Fmo* = *Fusarium monoliforme*. Fully conserved residues are boxed in red; the three catalytic aspartates are marked with ▲. Secondary structure elements are coded as follows: α = α-helix, β = β-strand, η = 310-helix, T = hydrogen bonded turn. Turns and loops lining the active site are indicated with their coil number and turn type.